

## SEQUENCE LISTING

Transal Control											
<110>	Figdor, Carl Gustav Geijtenbeek, Teunis Bernard Herman Van Kooyk, Yvette Torensma, Ruurd										
<120>	COMPOSITION AND METHOD FOR MODULATING DENDRITIC CELL-T CELL INTERACTION										
<130>	89 DIV										
<140> <141>	US 10/625,202 2003-07-23										
<150> <151>	09/719,961 2001-09-24										
	PCT/NL00/00253 2000-04-19										
	US 60/176,924 2000-01-20										
	EP 99201204.7 1999-04-19										
<160>	2										
<170>	PatentIn version 3.2										
<210> <211> <212> <213>	1215										
<220> <221> <222>	CDS (1)(1215)										
	l t gac tcc aag gaa cca aga ctg cag ctg ggc ctc ctg gag 4 r Asp Ser Lys Glu Pro Arg Leu Gln Gln Leu Gly Leu Leu Glu 5 10 15	8									
	a cag ctg aga ggc ctt gga ttc cga cag act cga gga tac aag u Gln Leu Arg Gly Leu Gly Phe Arg Gln Thr Arg Gly Tyr Lys 20 25 30	6									
	a gca ggg tgt ctt ggc cat ggt ccc ctg gtg ctg caa ctc ctc 14 u Ala Gly Cys Leu Gly His Gly Pro Leu Val Leu Gln Leu Leu 35 40 45	4									
tcc ttc Ser Pho	c acg ctc ttg gct ggg ctc ctt gtc caa gtg tcc aag gtc ccc 19 e Thr Leu Leu Ala Gly Leu Leu Val Gln Val Ser Lys Val Pro 55 60	2									

agc Ser 65	tcc Ser	ata Ile	agt Ser	cag Gln	gaa Glu 70	caa Gln	tcc Ser	agg Arg	caa Gln	gac Asp 75	gcg Ala	atc Ile	tac Tyr	cag Gln	aac Asn 80	240
ctg Leu	acc Thr	cag Gln	ctt Leu	aaa Lys 85	gct Ala	gca Ala	gtg Val	ggt Gly	gag Glu 90	ctc Leu	tca Ser	gag Glu	aaa Lys	tcc Ser 95	aag Lys	288
ctg Leu	cag Gln	gag Glu	atc Ile 100	tac Tyr	cag Gln	gag Glu	ctg Leu	acc Thr 105	cag Gln	ctg Leu	aag Lys	gct Ala	gca Ala 110	gtg Val	ggt Gly	336
gag Glu	ctt Leu	cca Pro 115	gag Glu	aaa Lys	tct Ser	aag Lys	ctg Leu 120	cag Gln	gag Glu	atc Ile	tac Tyr	cag Gln 125	gag Glu	ctg Leu	acc Thr	384
cgg Arg	ctg Leu 130	aag Lys	gct Ala	gca Ala	gtg Val	ggt Gly 135	gag Glu	ctt Leu	cca Pro	gag Glu	aaa Lys 140	tct Ser	aag Lys	ctg Leu	cag Gln	432
gag Glu 145	atc Ile	tac Tyr	cag Gln	gag Glu	ctg Leu 150	acc Thr	tgg Trp	ctg Leu	aag Lys	gct Ala 155	gca Ala	gtg Val	ggt Gly	gag Glu	ctt Leu 160	480
cca Pro	gag Glu	aaa Lys	tct Ser	aag Lys 165	atg Met	cag Gln	gag Glu	atc Ile	tac Tyr 170	cag Gln	gag Glu	ctg Leu	act Thr	cgg Arg 175	ctg Leu	528
aag Lys	gct Ala	gca Ala	gtg Val 180	ggt Gly	gag Glu	ctt Leu	cca Pro	gag Glu 185	aaa Lys	tct Ser	aag Lys	cag Gln	cag Gln 190	gag Glu	atc Ile	576
tac Tyr	cag Gln	gag Glu 195	ctg Leu	acc Thr	cgg Arg	ctg Leu	aag Lys 200	gct Ala	gca Ala	gtg Val	ggt Gly	gag Glu 205	ctt Leu	cca Pro	gag Glu	624
aaa Lys	tct Ser 210	aag Lys	cag Gln	cag Gln	gag Glu	atc Ile 215	Tyr	cag Gln	gag Glu	ctg Leu	acc Thr 220	cgg Arg	ctg Leu	aag Lys	gct Ala	672
gca Ala 225	gtg Val	ggt Gly	gag Glu	ctt Leu	cca Pro 230	gag Glu	aaa Lys	tct Ser	aag Lys	cag Gln 235	cag Gln	gag Glu	atc Ile	tac Tyr	cag Gln 240	720
gag Glu	ctg Leu	acc Thr	cag Gln	ctg Leu 245	aag Lys	gct Ala	gca Ala	gtg Val	gaa Glu 250	cgc Arg	ctg Leu	tgc Cys	cac His	ccc Pro 255	tgt Cys	768
ccc Pro	tgg Trp	gaa Glu	tgg Trp 260	aca Thr	ttc Phe	ttc Phe	caa Gln	gga Gly 265	aac Asn	tgt Cys	tac Tyr	ttc Phe	atg Met 270	tct Ser	aac Asn	816
tcc Ser	cag Gln	cgg Arg 275	aac Asn	tgg Trp	cac His	gac Asp	tcc Ser 280	atc Ile	acc Thr	gcc Ala	tgc Cys	aaa Lys 285	gaa Glu	gtg Val	ggg Gly	864

gcc cag ctc gtc gta atc aaa agt gct gag gag cag aac ttc cta cag Ala Gln Leu Val Val Ile Lys Ser Ala Glu Glu Gln Asn Phe Leu Gln 290 295 300	912										
ctg cag tct tcc aga agt aac cgc ttc acc tgg atg gga ctt tca gat Leu Gln Ser Ser Arg Ser Asn Arg Phe Thr Trp Met Gly Leu Ser Asp 305 310 315 320	960										
cta aat cag gaa ggc acg tgg caa tgg gtg gac ggc tca cct ctg ttg Leu Asn Gln Glu Gly Thr Trp Gln Trp Val Asp Gly Ser Pro Leu Leu 325 330 335	1008										
ccc agc ttc aag cag tat tgg aac aga gga gag ccc aac aac gtt ggg Pro Ser Phe Lys Gln Tyr Trp Asn Arg Gly Glu Pro Asn Asn Val Gly 340 345 350	1056										
gag gaa gac tgc gcg gaa ttt agt ggc aat ggc tgg aac gac gac aaa Glu Glu Asp Cys Ala Glu Phe Ser Gly Asn Gly Trp Asn Asp Asp Lys 355 360 365	1104										
tgt aat ctt gcc aaa ttc tgg atc tgc aaa aag tcc gca gcc tcc tgc Cys Asn Leu Ala Lys Phe Trp Ile Cys Lys Lys Ser Ala Ala Ser Cys 370 375 380	1152										
tcc agg gat gaa gaa cag ttt ctt tct cca gcc cct gcc acc cca aac Ser Arg Asp Glu Glu Gln Phe Leu Ser Pro Ala Pro Ala Thr Pro Asn 385 390 395 400	1200										
ccc cct cct gcg tag Pro Pro Pro Ala	1215										
<210> 2 <211> 404 <212> PRT <213> Homo sapiens											
<400> 2											
Met Ser Asp Ser Lys Glu Pro Arg Leu Gln Gln Leu Gly Leu Glu 1 5 10 15											
Glu Glu Gln Leu Arg Gly Leu Gly Phe Arg Gln Thr Arg Gly Tyr Lys 20 25 30											
Ser Leu Ala Gly Cys Leu Gly His Gly Pro Leu Val Leu Gln Leu Leu 35 40 45											

Ser Phe Thr Leu Leu Ala Gly Leu Leu Val Gln Val Ser Lys Val Pro 50 55 60

Ser Ser Ile Ser Gln Glu Gln Ser Arg Gln Asp Ala Ile Tyr Gln Asn 65 70 75 80

Leu Thr Gln Leu Lys Ala Ala Val Gly Glu Leu Ser Glu Lys Ser Lys 85 90 95

Leu Gl<br/>n Glu Ile Tyr Gl<br/>n Glu Leu Thr Gl<br/>n Leu Lys Ala Ala Val Gly 100 105 110

Glu Leu Pro Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr 115 120 125

Arg Leu Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln 130 135 140

Glu Ile Tyr Gln Glu Leu Thr Trp Leu Lys Ala Ala Val Gly Glu Leu 145 150 155 160

Pro Glu Lys Ser Lys Met Gln Glu Ile Tyr Gln Glu Leu Thr Arg Leu 165 170 175

Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Gln Gln Glu Ile 180 185 190

Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala Val Gly Glu Leu Pro Glu 195 200 205

Lys Ser Lys Gln Glu Ile Tyr Gln Glu Leu Thr Arg Leu Lys Ala 210 215 220

Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Gln Gln Glu Ile Tyr Gln 225 230 235 240

Glu Leu Thr Gln Leu Lys Ala Ala Val Glu Arg Leu Cys His Pro Cys 245 250 255

Pro Trp Glu Trp Thr Phe Phe Gln Gly Asn Cys Tyr Phe Met Ser Asn 260 265 270

Ser Gln Arg Asn Trp His Asp Ser Ile Thr Ala Cys Lys Glu Val Gly 275 280 285

Ala Gln Leu Val Val Ile Lys Ser Ala Glu Glu Gln Asn Phe Leu Gln 290 295 300

Leu Gln Ser Ser Arg Ser Asn Arg Phe Thr Trp Met Gly Leu Ser Asp 305 310 315 320

Leu Asn Gln Glu Gly Thr Trp Gln Trp Val Asp Gly Ser Pro Leu Leu 325 330 335

Pro Ser Phe Lys Gln Tyr Trp Asn Arg Gly Glu Pro Asn Asn Val Gly 340 345 350

Glu Glu Asp Cys Ala Glu Phe Ser Gly Asn Gly Trp Asn Asp Asp Lys 355 360 365

Cys Asn Leu Ala Lys Phe Trp Ile Cys Lys Lys Ser Ala Ala Ser Cys 370 375 380

Ser Arg Asp Glu Glu Gln Phe Leu Ser Pro Ala Pro Ala Thr Pro Asn 385 390 395 400

Pro Pro Pro Ala